

## SEQUENCE LISTING

<110> DARROW, ANDREW

QI, JENSON

ANDRADE-GORDON, PATRICIA

<120> ZYMOGEN ACTIVATION SYSTEM

<130> ORT-1028

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<160> 60

<170> PATENTIN VER. 2.0

<210> 1

<211> 361

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE

VECTORS.

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GAATTCACCA CCATGGACAG CAAAGGTCG TCGCAGAAAT CCCGCCTGCT CCTGCTGCTG 60

GTGGTGTCAA ATCTACTCTT GTGCCAGGGT GTGGTCTCCG ACTACAAGGA CGACGACGAC 120

GTGGACGCGG CCGCTCTTGC TGCCCCCTTT GATGATGATG ACAAGATCGT TGGGGCTAT 180

GCTCTAGATA GCGGCCGCTT CCCTTAGTG AGGGTTAATG CTTCGAGCAG ACATGATAAG 240

ATACATTGAT GAGTTGGAC AAACCACAAC TAGAATGCAG TGAAAAAAAT GCTTTATTG 300

TGAAATTTGT GATGCTATTG CTTTATTGT AACCAATTATA AGCTGCAATA AACAAAGTTGA 360

C

361

<210> 2

<211> 301

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE

VECTORS.

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GAATTCACCA TGAATCCACT CCTGATCCTT ACCTTTGTGG CGGCCGCTCT TGCTGCC 60

TTTGATGATG ATGACAAGAT CGTTGGGGC TATTGTCTAG ATACCCCTAC GATGTGCCG 120

ATTACGCCTA GC GGCCGCTT CCCTTAGTG AGGGTTAACG CTTCGAGCAG ACATGATAAG 180

ATACATTGAT GAGTTGGAC AAACCACAAAC TAGAATGCAG TGAAAAAAAT GCTTTATTG 240

TGAAATTGT GATGCTATTG CTTTATTGT AACCATTATA AGCTGCAATA AACAAAGTTGA 300

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301

<210> 3

<211> 484

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE

VECTORS.

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GTGGTGTCAA ATCTACTCTT GTGCCAGGGT GTGGTCTCCG ACTACAAGGA CGACGACGAC 120

GTGGACGCGG CCGCTCTTGC TGCCCCCTTT ATCGAGGGGC GCATTGTGGA GGGCTCGGAT 180

CTAGATAACCC CTACGATGTG CCCGATTACG CCGCTAGATA CCCCTACGAT GTGCCCGATT 240

ACGCCGCTAG ATACCAC TAC GATGTGCCCG ATTACGCCGC TAGATAACCC TACGATGTGC 300

CCGATTACGC CTAGCGGCCG CTTCCCTTTA GTGAGGGTTA ATGCTTCGAG CAGACATGAT 360

AAGATAACATT GATGAGTTTG GACAAACAC AACTAGAACATG CAGTGAAAAA AATGCTTTAT 420

TTGTGAAATT TGTGATGCTA TTGCTTTATT TGTAACCATT ATAAGCTGCA ATAAACAAGT 480

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<210> 4

<211> 382

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE

VECTORS.

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GTGGTGTCAA ATCTACTCTT GTGCCAGGGT GTGGTCTCCG ACTACAAGGA CGACGACGAC 120

GTGGACGCGG CCGCTCTTGC TGCCCCCTTT GATGATGATG ACAAGATCGT TGGGGCTAC 180

AACTGTCTAG ACATCACCAT CACCATCACT AGCGGCCGCT TCCCTTAGT GAGGGTTAAT 240

GCTTCGAGCA GACATGATAA GATACATTGA TGAGTTGGA CAAACCACAA CTAGAATGCA 300

GTGAAAAAAA TGCTTATTT GTGAAATTG TGATGCTATT GCTTTATTTG TAACCATTAT 360

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<210> 5

<211> 352

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE

VECTORS.

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TTCGGCTGCG GGGTCCCCGA CTACAAGGAC GACGACGACG CGGCCGCTCT TGCTGCCCCC 120

TTTGATGATG ATGACAAGAT CGTTGGGGC TATGCTCTAG ACATCACCAT CACCATCACT 180

AGCGGCCGCT TCCCTTTAGT GAGGGTTAAT GCTTCGAGCA GACATGATAA GATACATTGA 240

TGAGTTGGA CAAACCACAA CTAGAATGCA GTGAAAAAAA TGCTTATTG TGAAATTG 300

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<210> 6

<211> 385

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE

VECTORS.

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TTCGGCTGCG GGGTCCCCGA CTACAAGGAC GACGACGACG CGGCCGCTCT TGCTGCCCG 120

TTTGATGATG ATGACAAGAT CGTTGGGGC TATGCTCTAG ATACCCCTAC GATGTGCCCG 180

ATTACGCCGC TAGACATCAC CATCACCATC ACTAGCGGCC GCTTCCCTTT AGTGAGGGTT 240

AATGCTTCGA GCAGACATGA TAAGATAACAT TGATGAGTTT GGACAAACCA CAACTAGAAT 300

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<211> 1169

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE

WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN

<400> 7

GAATTCACCA CCATGGACAG CAAAGGTTCG TCGCAGAAAT CCCGCCTGCT CCTGCTGCTG 60

GTGGTGTCAA ATCTACTCTT GTGCCAGGGT GTGGTCTCCG ACTACAAGGA CGACGACGAC 120

GTGGACGCGG CCGCTCTTGC TGCCCCCTTT GATGATGATG ACAAGATCGT TGGGGCTAT 180

GCTCTAGAGG CCGGTCACTG GCCCTGGCAG GTCAGCATCA CCTATGAAGG CGTCCATGTG 240

TGTGGTGGCT CTCTCGTGTC TGAGCAGTGG GTGCTGTCAG CTGCTCACTG CTTCCCCAGC 300

GAGCACCACA AGGAAGCCTA TGAGGTCAAG CTGGGGGCC ACCAGCTAGA CTCCTACTCC 360

GAGGACGCCA AGGTCAAGCAC CCTGAAGGAC ATCATCCCC ACCCCAGCTA CCTCCAGGAG 420

GGCTCCCAGG GCGACATTGC ACTCCTCCAA CTCAGCAGAC CCATCACCTT CTCCCGCTAC 480

ATCCGGCCCA TCTGCCTCCC TGCAGCCAAC GCCTCCTTCC CCAACGGCCT CCACTGCACT 540

GTCACTGGCT GGGGTCATGT GGCCCCCTCA GTGAGCCTCC TGACGCCAA GCCACTGCAG 600  
CAACTCGAGG TGCCTCTGAT CAGTCGTGAG ACGTGTAACT GCCTGTACAA CATCGACGCC 660  
AAGCCTGAGG AGCCGCAC TT TGTCCAAGAG GACATGGTGT GTGCTGGCTA TGTGGAGGGG 720  
GGCAAGGACG CCTGCCAGGG TGACTCTGGG GGCCCAC TCT CCTGCCCTGT GGAGGGTCTC 780  
TGGTACCTGA CGGGCATTGT GAGCTGGGA GATGCCTGTG GGGCCCGCAA CAGGCCTGGT 840  
GTGTACACTC TGGCCTCCAG CTATGCCTCC TGGATCCAAA GCAAGGTGAC AGAACTCCAG 900  
CCTCGTGTGG TGCCCCAAC CCAGGAGTCC CAGCCCGACA GCAACCTCTG TGGCAGGCCAC 960  
CTGGCCTTCA GCTCTAGACA TCACCATCAC CATCACTAGC GGCGCTTCC CTTTAGTGAG 1020  
GGTTAATGCT TCGAGCAGAC ATGATAAGAT ACATTGATGA GTTTGGACAA ACCACAAC 1080  
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CCATTATAAG CTGCAATAAA CAAGTTGAC 1169

<210> 8

<211> 1142

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE

WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN

<400> 8

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TTCGGCTGCG GGGTCCCCGA CTACAAGGAC GACGACGACG CGGCCGCTCT TGCTGCCCCC 120  
TTTGATGATG ATGACAAGAT CGTTGGGGC TATGCTCTAG AGGCCGGTCA GTGGCCCTGG 180  
CAGGTCAGCA TCACCTATGA AGGCGTCCAT GTGTGTGGTG GCTCTCTCGT GTCTGAGCAG 240  
TGGGTGCTGT CAGCTGCTCA CTGCTTCCCC AGCGAGCACC ACAAGGAAGC CTATGAGGTC 300  
AAGCTGGGGG CCCACCAGCT AGACTCCTAC TCCGAGGACG CCAAGGTCAAG CACCTGAAG 360  
GACATCATCC CCCACCCAG CTACCTCCAG GAGGGCTCCC AGGGCGACAT TGCACTCCTC 420  
CAAECTCAGCA GACCCATCAC CTTCTCCGC TACATCCGGC CCATCTGCCT CCCTGCAGCC 480  
AACGCCTCCT TCCCCAACGG CCTCCACTGC ACTGTCACTG GCTGGGTCA TGTGGCCCCC 540  
TCAGTGAGCC TCCTGACGCC CAAGCCACTG CAGCAACTCG AGGTGCCTCT GATCAGTCGT 600  
GAGACGTGTA ACTGCCTGTA CAACATCGAC GCCAAGCCTG AGGAGCCGCA CTTTGTCCAA 660  
GAGGACATGG TGTGTGCTGG CTATGTGGAG GGGGGCAAGG ACGCCTGCCA GGGTGACTCT 720  
GGGGGCCAC TCTCCTGCC C TGTGGAGGGT CTCTGGTACC TGACGGCAT TGTGAGCTGG 780  
GGAGAGATGCCT GTGGGGCCCG CAACAGGCCT GGTGTGTACA CTCTGGCCTC CAGCTATGCC 840

TCCTGGATCC AAAGCAAGGT GACAGAACTC CAGCCTCGTG TGGTGCCCCA AACCCAGGAG 900

TCCCAGCCCC ACAGCAACCT CTGTGGCAGC CACCTGGCCT TCAGCTCTAG ACATCACCAT 960

CACCATCACT AGCGGCCGCT TCCCTTTAGT GAGGGTTAAT GCTTCGAGCA GACATGATAA 1020

GATACATTGA TGAGTTTGGG CAAACCACAA CTAGAATGCA GTGAAAAAAA TGCTTTATTT 1080

GTGAAATTTG TGATGCTATT GCTTTATTTG TAACCATTAT AAGCTGCAAT AAACAAGTTG 1140

AC 1142

<210> 9

<211> 1049

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE

WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN

<400> 9

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GTGGTGTCAA ATCTACTCTT GTGCCAGGGT GTGGTCTCCG ACTACAAGGA CGACGACGAC 120  
GTGGACGCGG CCGCTCTTGC TGCCCCCTTT GATGATGATG ACAAGATCGT TGGGGGCTAC 180  
AACTGTCTAG AACCCCATTG GCAGCCTTGG CAGGCGGCCT TGTTCCAGGG CCAGCAACTA 240  
CTCTGTGGCG GTGTCCCTGT AGGTGGCAAC TGGTCCTTA CAGCTGCCCA CTGTAAAAAA 300  
CCGAAATACA CAGTACGCCT GGGAGACCAC AGCCTACAGA ATAAAGATGG CCCAGAGCAA 360  
GAAATACTG TGGTCAGTC CATCCCACAC CCCTGCTACA ACAGCAGCGA TGTGGAGGAC 420  
CACAAACCATG ATCTGATGCT TCTTCAACTG CGTGACCAGG CATCCCTGGG GTCCAAAGTG 480  
AAGCCCATCA GCCTGGCAGA TCATTGCACC CAGCCTGGCC AGAAGTGCAC CGTCTCAGGC 540  
TGGGGCACTG TCACCACTG CCGAGAGAAT TTTCTGACA CTCTCAACTG TGCAGAAGTA 600  
AAAATTTTC CCCAGAAGAA GTGTGAGGAT GCTTACCCGG GGCAGATCAC AGATGGCATG 660  
GTCTGTGCAG GCAGCAGCAA AGGGGCTGAC ACGTGCCAGG GCGATTCTGG AGGCCCCCTG 720  
GTGTGTGATG GTGCACTCCA GGGCATCAC ACGTACCTGG CAGACCCCTG TGGGAGGTCC 780  
GACAAACCTG GCGTCTATAAC CAACATCTGC CGCTACCTGG ACTGGATCAA GAAGATCATA 840  
GGCAGCAAGG GCTCTAGACA TCACCATCAC CATCACTAGC GGCGCTTCC CTTTAGTGAG 900  
GGTTAATGCT TCGAGCAGAC ATGATAAGAT ACATTGATGA GTTTGGACAA ACCACAAC 960  
GAATGCAGTG AAAAAAATGC TTTATTGTG AAATTTGTGA TGCTATTGCT TTATTTGTAA 1020  
CCATTATAAG CTGCAATAAA CAAGTTGAC 1049

<210> 10

<211> 1052

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE

WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN

<400> 10

GAATTCACCA CCATGGACAG CAAAGGTTCG TCGCAGAAAT CCCGCCTGCT CCTGCTGCTG 60

GTGGTGTCAA ATCTACTCTT GTGCCAGGGT GTGGTCTCCG ACTACAAGGA CGACGACGAC 120

GTGGACGCGG CCGCTCTTGC TGCCCCCTTT GATGATGATG ACAAGATCGT TGGGGCTAC 180

AACTGTCTAG AAAAGCACTC CCAGCCCTGG CAGGCAGCCC TGTCGAGAA GACCGGGCTA 240

CTCTGTGGGG CGACGCTCAT CGCCCCCAGA TGGCTCCTGA CAGCAGCCCA CTGCCTCAAG 300

CCCCGCTACA TAGTTCACCT GGGGCAGCAC AACCTCCAGA AGGAGGAGGG CTGTGAGCAG 360

ACCCGGACAG CCACTGAGTC CTTCCCCAC CCCGGCTTCA ACAACAGCCT CCCCAACAAA 420

GACCACCGCA ATGACATCAT GCTGGTGAAG ATGGCATCGC CAGTCTCCAT CACCTGGGCT 480

GTGCGACCCC TCACCCTCTC CTCACGCTGT GTCACTGCTG GCACCAGCTG CCTCATTCC 540  
GGCTGGGCAGCAG CCCCCAGTTA CGCCTGCCTC ACACCTTGCG ATGCGCCAAC 600  
ATCACCATCA TTGAGCACCA GAAGTGTGAG AACGCCTACC CCGGCAACAT CACAGACACC 660  
ATGGTGTGTG CCAGCGTGCA GGAAGGGGGC AAGGACTCCT GCCAGGGTGA CTCCGGGGC 720  
CCTCTGGTCT GTAACCAGTC TCTTCAAGGC ATTATCTCCT GGGGCCAGGA TCCGTGTGCG 780  
ATCACCCGAA AGCCTGGTGT CTACACGAAA GTCTGCAAAT ATGTGGACTG GATCCAGGAG 840  
ACGATGAAGA ACAATTCTAG ACATCACCAT CACCATCACT AGCGGCCGCT TCCCTTTAGT 900  
GAGGGTTAAC GCTTCGAGCA GACATGATAA GATACATTGA TGAGTTTGGAA CAAACCACAA 960  
CTAGAATGCA GTGAAAAAAA TGCTTTATTT GTGAAATTG TGATGCTATT GCTTTATTG 1020  
TAACCATTAT AAGCTGCAAT AAACAAGTTG AC 1052

<210> 11

<211> 328

<212> PRT

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE

## WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN

&lt;400&gt; 11

MET ASP SER LYS GLY SER SER GLN LYS SER ARG LEU LEU LEU LEU

1 5 10 15

VAL VAL SER ASN LEU LEU LEU CYS GLN GLY VAL VAL SER ASP TYR LYS

20 25 30

ASP ASP ASP ASP VAL ASP ALA ALA ALA LEU ALA ALA PRO PHE ASP ASP

35 40 45

ASP ASP LYS ILE VAL GLY GLY TYR ALA LEU GLU ALA GLY GLN TRP PRO

50 55 60

TRP GLN VAL SER ILE THR TYR GLU GLY VAL HIS VAL CYS GLY GLY SER

65 70 75 80

LEU VAL SER GLU GLN TRP VAL LEU SER ALA ALA HIS CYS PHE PRO SER

85

90

95

GLU HIS HIS LYS GLU ALA TYR GLU VAL LYS LEU GLY ALA HIS GLN LEU

100

105

110

ASP SER TYR SER GLU ASP ALA LYS VAL SER THR LEU LYS ASP ILE ILE

115

120

125

PRO HIS PRO SER TYR LEU GLN GLU GLY SER GLN GLY ASP ILE ALA LEU

130

135

140

LEU GLN LEU SER ARG PRO ILE THR PHE SER ARG TYR ILE ARG PRO ILE

145

150

155

160

CYS LEU PRO ALA ALA ASN ALA SER PHE PRO ASN GLY LEU HIS CYS THR

165

170

175

80

VAL THR GLY TRP GLY HIS VAL ALA PRO SER VAL SER LEU LEU THR PRO

180

185

190

LYS PRO LEU GLN GLN LEU GLU VAL PRO LEU ILE SER ARG GLU THR CYS

195

200

205

ASN CYS LEU TYR ASN ILE ASP ALA LYS PRO GLU GLU PRO HIS PHE VAL

210

215

220

GLN GLU ASP MET VAL CYS ALA GLY TYR VAL GLU GLY GLY LYS ASP ALA

225

230

235

240

CYS GLN GLY ASP SER GLY GLY PRO LEU SER CYS PRO VAL GLU GLY LEU

245

250

255

TRP TYR LEU THR GLY ILE VAL SER TRP GLY ASP ALA CYS GLY ALA ARG

260

265

270

ASN ARG PRO GLY VAL TYR THR LEU ALA SER SER TYR ALA SER TRP ILE

275

280

285

GLN SER LYS VAL THR GLU LEU GLN PRO ARG VAL VAL PRO GLN THR GLN

290

295

300

GLU SER GLN PRO ASP SER ASN LEU CYS GLY SER HIS LEU ALA PHE SER

305

310

315

320

SER ARG HIS HIS HIS HIS HIS

325

<210> 12

<211> 319

<212> PRT

<213> ARTIFICIAL SEQUENCE

&lt;220&gt;

&lt;223&gt; DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE

WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN

&lt;400&gt; 12

MET ALA PHE LEU TRP LEU LEU SER CYS TRP ALA LEU LEU GLY THR THR

1 5 10 15

PHE GLY CYS GLY VAL PRO ASP TYR LYS ASP ASP ASP ASP ALA ALA ALA

20 25 30

LEU ALA ALA PRO PHE ASP ASP ASP ASP LYS ILE VAL GLY GLY TYR ALA

35 40 45

LEU GLU ALA GLY GLN TRP PRO TRP GLN VAL SER ILE THR TYR GLU GLY

50 55 60

VAL HIS VAL CYS GLY GLY SER LEU VAL SER GLU GLN TRP VAL LEU SER

65

70

75

80

ALA ALA HIS CYS PHE PRO SER GLU HIS HIS LYS GLU ALA TYR GLU VAL

85

90

95

LYS LEU GLY ALA HIS GLN LEU ASP SER TYR SER GLU ASP ALA LYS VAL

100

105

110

SER THR LEU LYS ASP ILE ILE PRO HIS PRO SER TYR LEU GLN GLU GLY

115

120

125

SER GLN GLY ASP ILE ALA LEU LEU GLN LEU SER ARG PRO ILE THR PHE

130

135

140

SER ARG TYR ILE ARG PRO ILE CYS LEU PRO ALA ALA ASN ALA SER PHE

145

150

155

160

PRO ASN GLY LEU HIS CYS THR VAL THR GLY TRP GLY HIS VAL ALA PRO

165

170

175

SER VAL SER LEU LEU THR PRO LYS PRO LEU GLN GLN LEU GLU VAL PRO

180

185

190

LEU ILE SER ARG GLU THR CYS ASN CYS LEU TYR ASN ILE ASP ALA LYS

195

200

205

PRO GLU GLU PRO HIS PHE VAL GLN GLU ASP MET VAL CYS ALA GLY TYR

210

215

220

VAL GLU GLY GLY LYS ASP ALA CYS GLN GLY ASP SER GLY GLY PRO LEU

225

230

235

240

SER CYS PRO VAL GLU GLY LEU TRP TYR LEU THR GLY ILE VAL SER TRP

245

250

255

GLY ASP ALA CYS GLY ALA ARG ASN ARG PRO GLY VAL TYR THR LEU ALA

85

260

265

270

SER SER TYR ALA SER TRP ILE GLN SER LYS VAL THR GLU LEU GLN PRO

275

280

285

ARG VAL VAL PRO GLN THR GLN GLU SER GLN PRO ASP SER ASN LEU CYS

290

295

300

GLY SER HIS LEU ALA PHE SER SER ARG HIS HIS HIS HIS HIS HIS

305

310

315

<210> 13

<211> 288

<212> PRT

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE

WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN

<400> 13

MET ASP SER LYS GLY SER SER GLN LYS SER ARG LEU LEU LEU LEU LEU

1 5 10 15

VAL VAL SER ASN LEU LEU LEU CYS GLN GLY VAL VAL SER ASP TYR LYS

20 25 30

ASP ASP ASP ASP VAL ASP ALA ALA ALA LEU ALA ALA PRO PHE ASP ASP

35 40 45

ASP ASP LYS ILE VAL GLY GLY TYR ASN CYS LEU GLU PRO HIS SER GLN

50 55 60

PRO TRP GLN ALA ALA LEU PHE GLN GLY GLN GLN LEU LEU CYS GLY GLY

65 70 75 80

VAL LEU VAL GLY GLY ASN TRP VAL LEU THR ALA ALA HIS CYS LYS LYS

85

90

95

PRO LYS TYR THR VAL ARG LEU GLY ASP HIS SER LEU GLN ASN LYS ASP

100

105

110

GLY PRO GLU GLN GLU ILE PRO VAL VAL GLN SER ILE PRO HIS PRO CYS

115

120

125

TYR ASN SER SER ASP VAL GLU ASP HIS ASN HIS ASP LEU MET LEU LEU

130

135

140

GLN LEU ARG ASP GLN ALA SER LEU GLY SER LYS VAL LYS PRO ILE SER

145

150

155

160

LEU ALA ASP HIS CYS THR GLN PRO GLY GLN LYS CYS THR VAL SER GLY

165

170

175

TRP GLY THR VAL THR SER PRO ARG GLU ASN PHE PRO ASP THR LEU ASN

180

185

190

CYS ALA GLU VAL LYS ILE PHE PRO GLN LYS LYS CYS GLU ASP ALA TYR

195

200

205

PRO GLY GLN ILE THR ASP GLY MET VAL CYS ALA GLY SER SER LYS GLY

210

215

220

ALA ASP THR CYS GLN GLY ASP SER GLY GLY PRO LEU VAL CYS ASP GLY

225

230

235

240

ALA LEU GLN GLY ILE THR SER TRP GLY SER ASP PRO CYS GLY ARG SER

245

250

255

ASP LYS PRO GLY VAL TYR THR ASN ILE CYS ARG TYR LEU ASP TRP ILE

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LYS LYS ILE ILE GLY SER LYS GLY SER ARG HIS HIS HIS HIS HIS

275

280

285

<210> 14

<211> 289

<212> PRT

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE

WITH HOMO SAPIEN SERINE PROTEASE CATALYTIC DOMAIN

<400> 14

90

MET ASP SER LYS GLY SER SER GLN LYS SER ARG LEU LEU LEU LEU

1

5

10

15

VAL VAL SER ASN LEU LEU LEU CYS GLN GLY VAL VAL SER ASP TYR LYS

20

25

30

ASP ASP ASP ASP VAL ASP ALA ALA ALA LEU ALA ALA PRO PHE ASP ASP

35

40

45

ASP ASP LYS ILE VAL GLY GLY TYR ASN CYS LEU GLU LYS HIS SER GLN

50

55

60

PRO TRP GLN ALA ALA LEU PHE GLU LYS THR ARG LEU LEU CYS GLY ALA

65

70

75

80

THR LEU ILE ALA PRO ARG TRP LEU LEU THR ALA ALA HIS CYS LEU LYS

85

90

95

PRO ARG TYR ILE VAL HIS LEU GLY GLN HIS ASN LEU GLN LYS GLU GLU

100

105

110

GLY CYS GLU GLN THR ARG THR ALA THR GLU SER PHE PRO HIS PRO GLY

115

120

125

PHE ASN ASN SER LEU PRO ASN LYS ASP HIS ARG ASN ASP ILE MET LEU

130

135

140

VAL LYS MET ALA SER PRO VAL SER ILE THR TRP ALA VAL ARG PRO LEU

145

150

155

160

THR LEU SER SER ARG CYS VAL THR ALA GLY THR SER CYS LEU ILE SER

165

170

175

GLY TRP GLY SER THR SER SER PRO GLN LEU ARG LEU PRO HIS THR LEU

180

185

190

ARG CYS ALA ASN ILE THR ILE ILE GLU HIS GLN LYS CYS GLU ASN ALA

195

200

205

TYR PRO GLY ASN ILE THR ASP THR MET VAL CYS ALA SER VAL GLN GLU

210

215

220

GLY GLY LYS ASP SER CYS GLN GLY ASP SER GLY GLY PRO LEU VAL CYS

225

230

235

240

ASN GLN SER LEU GLN GLY ILE ILE SER TRP GLY GLN ASP PRO CYS ALA

245

250

255

ILE THR ARG LYS PRO GLY VAL TYR THR LYS VAL CYS LYS TYR VAL ASP

260

265

270

TRP ILE GLN GLU THR MET LYS ASN ASN SER ARG HIS HIS HIS HIS

275

280

285

HIS

<210> 15

<211> 9

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 15

CTAGATAGC

9

<210> 16

<211> 9

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<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 16

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<210> 17

<211> 36

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

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36

<210> 18

<211> 36

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

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36

<210> 19

<211> 33

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

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<210> 20

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<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 20

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<210> 21

<211> 27

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 21

CTAGACATCA CCATCACCAT CACTAGC

27

<210> 22

<211> 27

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 22

GGCCGCTAGT GATGGTGATG GTGATGT

27

<210> 23

<211> 34

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 23

TGAATTCA CCACCATGGACA GCAAAGGTTC GTCG

34

<210> 24

<211> 30

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 24

CAGAAAGGGT CCCGCCTGCT CCTGCTGCTG

30

<210> 25

<211> 30

100

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 25

GTGGTGTCAA ATCTACTCTT GTGCCAGGGT

30

<210> 26

<211> 30

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 26

GTGGTCTCCG ACTACAAGGA CGACGACGAC

30

<210> 27

<211> 21

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 27

GTGGACGCGG CCGCATTATT A

21

<210> 28

<211> 35

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 28

TAATAATGCG GCCGCGTCCA CGTCGTCGTC GTCT

35

<210> 29

<211> 21

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

103

<400> 29

TGTAGTCGGA GACCACACCC T

21

<210> 30

<211> 30

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 30

GGCACAAAGAG TAGATTTGAC ACCACCAGCA

30

<210> 31

<211> 30

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 31

GCAGGAGCAG GCGGGACCCT TTCTGCGACG

30

<210> 32

<211> 29

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

105

<400> 32

AACCTTGCT GTCCATGGTG GTGAATTCA

29

<210> 33

<211> 40

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 33

AATTCACCAT GAATCCACTC CTGATCCTTA CCTTTGTGGC

40

<210> 34

<211> 40

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 34

GGCCGCCACA AAGGTAAGGA TCAGGAGTGG ATTCA

TGGTG

40

<210> 35

<211> 55

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 35

AATTCACCAAC CATGGCTTTC CTCTGGCTCC TCTCCTGCTG GGCCCTCCTG GGTAC 55

<210> 36

<211> 47

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 36

CCAGGAGGGC CCAGCAGGAG AGGAGCCAGA GGAAAGCCAT GGTGGTG

47

<210> 37

<211> 45

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 37

CACCTTCGGC TGCGGGGTCC CCGACTACAA GGACGACGAC GACGC

45

<210> 38

<211> 53

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 38

GGCCGGCTCG TCGTCGT CCT TGTAGTCGGG GACCCCGCAG CCGAAGGTGG TAC 53

<210> 39

<211> 29

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 39

GTGGCGGCCG CTCTTGCTGC CCCCTTTGA 29

<210> 40

<211> 28

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 40

TTCTCTAGAC AGTTGTAGCC CCCAACGA

28

<210> 41

<211> 55

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 41

GGCCGCTCTT GCTGCCCTTGATGATGA TGACAAGATC GTTGGGGCT ATGCT 55

<210> 42

<211> 55

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 42

CTAGAGCATA GCCCCAACG ATCTTGTCA CATCATCAA GGGGCAGCA AGAGC 55

<210> 43

<211> 55

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 43

GGCCGCTCTT GCTGCCCT TGATGATGA TGACAAGATC GTTGGGGCT ATTGT 55

<210> 44

<211> 55

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 44

CTAGACAATA GCCCCCAACG ATCTTGTCA CATCATCAA GGGGGCAGCA AGAGC 55

<210> 45

<211> 52

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 45

GGCCGCTCTT GCTGCCCTT TTATCGAGGG GCGCATTGTG GAGGGCTCGG AT 52

<210> 46

<211> 52

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 46

CTAGATCCGA GCCCTCCACA ATGCGCCCCT CGATAAAGGG GGCAGCAAGA GC

52

<210> 47

<211> 32

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 47

AGCAGTCTAG AGGCCGGTCA GTGGCCCTGG CA

32

<210> 48

<211> 28

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 48

GCTGGTCTAG AGCTGAAGGC CAGGTGGC

28

<210> 49

<211> 29

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 49

GGTATCTAGA GCCCTTGCTG CCTATGATC

29

<210> 50

<211> 30

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 50

ACTGTCTAGA ACCCCATTG CAGCCTTGGC

30

<210> 51

<211> 32

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 51

TCGATCTAGA AAAGCACTCC CAGCCCTGGC AG

32

<210> 52

<211> 32

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE:

OLIGONUCLEOTIDE

<400> 52

GTCCTCTAGA ATTGTTCTTC ATCGTCTCCT GG

32

<210> 53

<211> 306

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: FUSION GENE OF

HUMAN PROTEASE F IN CFEK2 ZYMOGEN VECTOR

&lt;400&gt; 53

MET ALA PHE LEU TRP LEU LEU SER CYS TRP ALA LEU LEU GLY THR THR

1 5 10 15

PHE GLY CYS GLY VAL PRO ASP TYR LYS ASP ASP ASP ASP ALA ALA ALA

20 25 30

LEU ALA ALA PRO PHE ASP ASP ASP ASP LYS ILE VAL GLY GLY TYR ALA

35 40 45

LEU GLU LEU GLY ARG TRP PRO TRP GLN GLY SER LEU ARG LEU TRP ASP

50 55 60

SER HIS VAL CYS GLY VAL SER LEU LEU SER HIS ARG TRP ALA LEU THR

65 70 75 80

ALA ALA HIS CYS PHE GLU THR TYR SER ASP LEU SER ASP PRO SER GLY

120

85

90

95

TRP MET VAL GLN PHE GLY GLN LEU THR SER MET PRO SER PHE TRP SER

100

105

110

LEU GLN ALA TYR TYR ASN ARG TYR PHE VAL SER ASN ILE TYR LEU SER

115

120

125

PRO ARG TYR LEU GLY ASN SER PRO TYR ASP ILE ALA LEU VAL LYS LEU

130

135

140

SER ALA PRO VAL THR TYR THR LYS HIS ILE GLN PRO ILE CYS LEU GLN

145

150

155

160

ALA SER THR PHE GLU PHE GLU ASN ARG THR ASP CYS TRP VAL THR GLY

165

170

175

TRP GLY TYR ILE LYS GLU ASP GLU ALA LEU PRO SER PRO HIS THR LEU

121

180

185

190

GLN GLU VAL GLN VAL ALA ILE ILE ASN ASN SER MET CYS ASN HIS LEU

195

200

205

PHE LEU LYS TYR SER PHE ARG LYS ASP ILE PHE GLY ASP MET VAL CYS

210

215

220

ALA GLY ASN ALA GLN GLY GLY LYS ASP ALA CYS PHE GLY ASP SER GLY

225

230

235

240

GLY PRO LEU ALA CYS ASN LYS ASN GLY LEU TRP TYR GLN ILE GLY VAL

245

250

255

VAL SER TRP GLY VAL GLY CYS GLY ARG PRO ASN ARG PRO GLY VAL TYR

260

265

270

THR ASN ILE SER HIS HIS PHE GLU TRP ILE GLN LYS LEU MET ALA GLN

122

275

280

285

SER GLY MET SER GLN PRO ASP PRO SER TRP SER ARG HIS HIS HIS

290

295

300

HIS HIS

305

<210> 54

<211> 284

<212> PRT

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: HUMAN MH2

PROTEASE IN PFEK ZYMOGEN VECTOR

&lt;400&gt; 54

MET ASP SER LYS GLY SER SER GLN LYS SER ARG LEU LEU LEU LEU LEU

1 5 10 15

VAL VAL SER ASN LEU LEU LEU CYS GLN GLY VAL VAL SER ASP TYR LYS

20 25 30

ASP ASP ASP ASP VAL ASP ALA ALA ALA LEU ALA ALA PRO PHE ASP ASP

35 40 45

ASP ASP LYS ILE VAL GLY GLY TYR ASN CYS LEU GLU PRO HIS SER GLN

50 55 60

PRO TRP GLN ALA ALA LEU VAL MET GLU ASN GLU LEU PHE CYS SER GLY

65 70 75 80

VAL LEU VAL HIS PRO GLN TRP VAL LEU SER ALA ALA HIS CYS PHE GLN

85 90 95

124

ASN SER TYR THR ILE GLY LEU GLY LEU HIS SER LEU GLU ALA ASP GLN

100

105

110

GLU PRO GLY SER GLN MET VAL GLU ALA SER LEU SER VAL ARG HIS PRO

115

120

125

GLU TYR ASN ARG PRO LEU LEU ALA ASN ASP LEU MET LEU ILE LYS LEU

130

135

140

ASP GLU SER VAL SER GLU SER ASP THR ILE ARG SER ILE SER ILE ALA

145

150

155

160

SER GLN CYS PRO THR ALA GLY ASN SER CYS LEU VAL SER GLY TRP GLY

165

170

175

LEU LEU ALA ASN GLY ARG MET PRO THR VAL LEU GLN CYS VAL ASN VAL

180

185

190

125

SER VAL VAL SER GLU GLU VAL CYS SER LYS LEU TYR ASP PRO LEU TYR

195

200

205

HIS PRO SER MET PHE CYS ALA GLY GLY GLY HIS ASP GLN LYS ASP SER

210

215

220

CYS ASN GLY ASP SER GLY GLY PRO LEU ILE CYS ASN GLY TYR LEU GLN

225

230

235

240

GLY LEU VAL SER PHE GLY LYS ALA PRO CYS GLY GLN VAL GLY VAL PRO

245

250

255

GLY VAL TYR THR ASN LEU CYS LYS PHE THR GLU TRP ILE GLU LYS THR

260

265

270

VAL GLN ALA SER SER ARG HIS HIS HIS HIS HIS HIS

275

280

126

<210> 55

<211> 30

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: PCR PRIMER

<400> 55

AGGATCTAGA GCCGCACTCG CAGCCCTGGC

30

<210> 56

<211> 30

<212> DNA

<213> ARTIFICIAL SEQUENCE

&lt;220&gt;

&lt;223&gt; DESCRIPTION OF ARTIFICIAL SEQUENCE: PCR PRIMER

&lt;400&gt; 56

CCCATCTAGA ACTGGCCTGG ACGGTTTCT

30

&lt;210&gt; 57

&lt;211&gt; 32

&lt;212&gt; DNA

&lt;213&gt; ARTIFICIAL SEQUENCE

&lt;220&gt;

&lt;223&gt; DESCRIPTION OF ARTIFICIAL SEQUENCE: PCR PRIMER

&lt;400&gt; 57

AGGATCTAGA ACTCGGGCGT TGGCCGTGGC AG

32

&lt;210&gt; 58

<211> 30

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: PCR PRIMER

<400> 58

AGAGTCTAGA CCAGGAGGGG TCTGGCTGGG

30

<210> 59

<211> 1103

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: NUCLEIC ACID

SEQUENCE OF HUMAN PROTEASE F IN CFEK2 ZYMOGEN

## VECTOR

&lt;400&gt; 59

GAATTCACCA CCATGGCTTT CCTCTGGCTC CTCTCCTGCT GGGCCCTCCT GGGTACCACC 60  
TTCGGCTGCG GGGTCCCCGA CTACAAGGAC GACGACGACG CGGCCGCTCT TGCTGCCCCC 120  
TTTGATGATG ATGACAAGAT CGTTGGGGC TATGCTCTAG AACTCGGGCG TTGGCCGTGG 180  
CAGGGGAGCC TGCGCCTGTG GGATTCCCAC GTATGCGGAG TGAGCCTGCT CAGCCACCGC 240  
TGGGCACTCA CGGCAGCGCA CTGCTTGAA ACCTATAGTG ACCTTAGTGA TCCCTCCGGG 300  
TGGATGGTCC AGTTTGGCCA GCTGACTTCC ATGCCATCCT TCTGGAGCCT GCAGGCCTAC 360  
TACAACCGTT ACTTCGTATC GAATATCTAT CTGAGCCCTC GCTACCTGGG GAATTCACCC 420  
TATGACATTG CCTTGGTGAA GCTGTCTGCA CCTGTCACCT ACACTAAACA CATCCAGCCC 480  
ATCTGTCTCC AGGCCTCCAC ATTTGAGTTT GAGAACCGGA CAGACTGCTG GGTGACTGGC 540  
TGGGGGTACA TCAAAGAGGA TGAGGCACTG CCATCTCCCC ACACCCCTCCA GGAAGTTCAAG 600  
GTCGCCATCA TAAACAACTC TATGTGCAAC CACCTCTTCC TCAAGTACAG TTTCCGCAAG 660  
GACATCTTG GAGACATGGT TTGTGCTGGC AATGCCAAG GCGGGAAGGA TGCCTGCTTC 720  
GGTGACTCAG GTGGACCCTT GGCCTGTAAC AAGAATGGAC TGTGGTATCA GATTGGAGTC 780  
GTGAGCTGGG GAGTGGGCTG TGGTCGGCCC AATCGGCCCG GTGTCTACAC CAATATCAGC 840  
CACCACTTTG AGTGGATCCA GAAGCTGATG GCCCAGAGTG GCATGTCCCA GCCAGACCCC 900

130

TCCTGGTCTA GACATCACCA TCACCATCAC TAGCGGCCGC TTCCCTTAG TGAGGGTAA 960

TGCTTCGAGC AGACATGATA AGATACATTG ATGAGTTGG ACAAACACACA ACTAGAATGC 1020

AGTGAAAAAA ATGCTTTATT TGTGAAATT GTGATGCTAT TGCTTTATTT GTAACCATTA 1080

TAAGCTGCAA TAAACAAGTT GAC

1103

<210> 60

<211> 1037

<212> DNA

<213> ARTIFICIAL SEQUENCE

<220>

<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: NUCLEIC ACID

SEQUENCE OF HUMAN MH2 PROTEASE IN PFEK ZYMOGEN

VECTOR

<400> 60

GAATTCACCA CCATGGACAG CAAAGGTCG TCGCAGAAAT CCCGCCTGCT CCTGCTGCTG 60

GTGGTGTCAA ATCTACTCTT GTGCCAGGGT GTGGTCTCCG ACTACAAGGA CGACGACGAC 120

GTGGACGCGG CCGCTCTTGC TGCCCCCTTT GATGATGATG ACAAGATCGT TGGGGGCTAC 180  
AACTGTCTAG AGCCGCACTC GCAGCCCTGG CAGGCGGCAC TGGTCATGGA AAACGAATTG 240  
TTCTGCTCGG GCGTCCTGGT GCATCCGCAG TGGGTGCTGT CAGCCGCACA CTGTTCCAG 300  
AACTCCTACA CCATCGGGCT GGGCCTGCAC AGTCTTGAGG CCGACCAAGA GCCAGGGAGC 360  
CAGATGGTGG AGGCCAGCCT CTCCGTACGG CACCCAGAGT ACAACAGACC CTTGCTCGCT 420  
AACGACCTCA TGCTCATCAA GTTGGACGAA TCCGTGTCCG AGTCTGACAC CATCCGGAGC 480  
ATCAGCATTG CTTCGCAGTG CCCTACCGCG GGGAACTCTT GCCTCGTTTC TGGCTGGGGT 540  
CTGCTGGCGA ACGGCAGAAT GCCTACCGTG CTGCAGTGCG TGAACGTGTC GGTGGTGTCT 600  
GAGGAGGTCT GCAGTAAGCT CTATGACCCG CTGTACCACC CCAGCATGTT CTGCGCCGGC 660  
GGAGGGCACG ACCAGAAGGA CT CCTGCAAC GGTGACTCTG GGGGGCCCT GATCTGCAAC 720  
GGGTACTTGC AGGGCCTTGT GTCTTCGGA AAAGCCCCGT GTGGCCAAGT TGGCGTGCCA 780  
GGTGTCTACA CCAACCTCTG CAAATTCACT GAGTGGATAG AGAAAACCGT CCAGGCCAGT 840  
TCTAGACATC ACCATCACCA TCACTAGCGG CCGCTTCCCT TTAGTGAGGG TTAATGCTTC 900  
GAGCAGACAT GATAAGATAC ATTGATGAGT TTGGACAAAC CACAACTAGA ATGCAGTGAA 960  
AAAAATGCTT TATTTGTGAA ATTTGTGATG CTATTGCTTT ATTTGTAACC ATTATAAGCT 1020  
GCAATAAACAA AGTTGAC